In the specification:

Please replace the paragraph starting at page 30, line 25, with the following paragraph:

In another preferred embodiment, the first functional subunit comprises at least one WD repeat, or at least a portion thereof sufficient for interaction with at least one other E3 component. The E3 recruiting domain may also contain at least two, at least three, at least four, at least five, at least six or any higher number of WD repeats from an E3 substrate binding component. For example, a Cdc4 polypeptide which lacks the three C-terminal WD repeats out of the seven WD repeats present in the protein, is capable of forming an E3 complex (Skowyra et al. (1997) *Cell* 91:209). The number of WD repeats that must be included in a chimeric protein of the invention, as well as which portion of the repeats must be included, can be determined as described in Skowyra or as further described herein). Preferred WD repeats for use in the invention are included in the h-βTrCP protein having SEQ ID No. 4. As described in Margollin et al., supra, the first WD repeat corresponds to amino acids 260-293, the second WD repeat corresponds to amino acids 305-333, the third WD repeat corresponds to amino acids [[245]] 345-373, the fourth WD repeat corresponds to amino acids 388-416; the fifth WD repeat corresponds to amino acids 428-456, the sixth WD repeat corresponds to amino acids 468-497; and the seventh WD repeat corresponds to amino acids 518-546 of the amino acid sequence of the h-βTrCP protein. The amino acid sequence of WD repeats of the *S. cerevisae* Met30p, *Neurospora crassa* Scon2p and the *Xenopus levi* proteins can also be found in Margollis et al., *supra*.

Please replace the paragraph starting at page 17, line 19, with the following paragraph:

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are identical at that position. A degree of homology or similarity or identity between nucleic acid sequences is a function of the number of identical or matching nucleotides at positions shared by the nucleic acid sequences. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid sequences is a function of the number of amino acids, i.e. structurally related, at positions shared by the amino acid sequences. An "unrelated" or "non-homologous" sequence shares less than 40 % identity, though preferably less than 25 % identity, with one of the [[ACE-2]] sequences of the present invention.

Please replace the paragraph starting at page 27, line 28, with the following paragraph:

There are many ways by which such libraries of potential homologs can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential [[ACE-2]] sequences. The synthesis of degenerate oligonucleotides is well known in the art (see for example, Narang, SA (1983) Tetrahedron 39:3; Itakura et al. (1981) Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules, ed. AG Walton, Amsterdam: Elsevier pp 273-289; Itakura et al. (1984) Annu. Rev. Biochem. 53:323; Itakura et al. (1984) Science 198:1056; Ike et al. (1983) Nucleic Acid Res. 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) Science 249:386-390; Roberts et al. (1992) PNAS 89:2429-2433; Devlin et al. (1990) Science 249: 404-406; Cwirla et al. (1990) PNAS 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Please replace the paragraph starting at page 121, line 4, with the following paragraph:

In some instances, it may be desirable to express ~~the~~ a recombinant [[ACE-2]] polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the ß-gal containing pBlueBac III).